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Genome characterization of two valuable therapeutic bacteriophages against *Salmonella* and *Campylobacter*

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Salmonella and *Campylobacter* are recognized worldwide as the major foodborne pathogens responsible for human gastrointestinal diseases. The increased resistance of bacteria to antibiotics has encouraged the development of alternatives to control bacterial pathogens. Bacteriophages (phages), as natural predators of bacteria, are considered an appealing option. We report herein the isolation and genome characterisation of two *Myoviridae* broad lytic spectra *Campylobacter* (vB_CcoM-IBB35) and *Salmonella* phages (PVP-SE1) with high potential for therapy. The majority of genes of vB_CcoM-IBB35 are unique although homology exists with members of the *Teequatrovirinae*. Unique genes involved in pathogenesis, carbohydrate and amino acid metabolism were also observed along with several incidences of gene duplications, split genes with intein and introns and “insertion-like sequences”.

From the 244 genes found in PVP-SE1, approximately 46% encode unique proteins and only 22.1% exhibited homology with known proteins. The genome sequence presents high homology (145 gene encoding proteins) with the *E.coli* bacteriophage rV5, both unrelated to any other known phage, which might suggest that they belong to a new phage genetic group. As conclusion, one can argue that the genomic characterization of both phages did not reveal any factor which could preclude its therapeutic use.

References

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